

Listing of Claims

This listing of claims will replace all prior versions and listings of claims in the application.

1. (CURRENTLY AMENDED) A method for measuring the amount of at least two target nucleic acid sequences in a biological sample, comprising the steps of:
 - a) preparing a sample by combining in a sample the biological sample comprising the at least two target nucleic acid sequences and a known amount of at least two standard nucleic acids, wherein said at least two standard nucleic acids have a nucleotide sequence that is one base different than the respective target nucleic acid sequence;
 - b) amplifying the sample of step a);
 - c) using ~~a further method~~ a primer extension reaction at the site of differentiation to enhance a mass difference between the at least two standard nucleic acid sequences and the at least two target nucleic acid sequences at the site wherein each of the standard nucleic acid sequence differs from the respective target nucleic acid sequence resulting in enhanced products with different masses so that the mass differences between the at least two standard and the at least two target nucleic acid sequences can be detected; and
 - d) quantifying the enhanced products of step c) by measuring the ratio of each of the amplified target nucleic acid to its corresponding amplified standard nucleic acid to measure the amount of the at least two target nucleic acid sequences present in the biological sample, wherein the quantifying is performed using MALDI-TOF mass spectrometry.
2. (PREVIOUSLY PRESENTED) The method of claim 1, wherein the at least two target nucleic acid sequences are from an infectious agent.

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3. (ORIGINAL) The method of claim 1, wherein the at least two target nucleic acid sequences are mRNA transcripts.
4. (CANCELLED)
5. (CANCELLED)
6. (CANCELLED)
7. (CANCELLED)
8. (CANCELLED)
9. (CANCELLED)
10. (PREVIOUSLY PRESENTED) The method of claim 1, wherein one measures the amount of at least 5 target nucleic acid sequences using at least 5 respective standard nucleic acids.
11. (PREVIOUSLY PRESENTED) The method of claim 1, wherein one measures the amount of at least 10 target nucleic acid sequences using at least 10 respective standard nucleic acids.
12. (PREVIOUSLY PRESENTED) The method of claim 1, wherein one measures the amount of 25 target nucleic acid sequences using at least 25 respective standard nucleic acids.
13. (PREVIOUSLY PRESENTED) The method of claim 1, wherein one measures the amount of 50 target nucleic acid sequences using at least 50 respective standard nucleic acids.

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14. (CANCELLED)